```
=> s screening potential drugs
L1          24 SCREENING POTENTIAL DRUGS

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2          13 DUP REM L1 (11 DUPLICATES REMOVED)

=> d abs, bib 1-13

L2   ANSWER 1 OF 13  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN   2002:111996  BIOSIS
DN   PREV200200111996
TI   Molecular and taxonomic diversity in drug discovery: Experience of
     chemical and biological screening approaches.
AU   Ainsworth, A. M. (1); Wrigley, S. K.; Fauth, U.
CS   (1) TerraGen Discovery (UK) Ltd., Slough: martyn.ainsworth@terragen.co.uk
     UK
SO   Pointing, Stephen B. [Editor]; Hyde, Kevin D. [Editor]. Fungal Diversity
     Research Series, (2001) No. 6, pp. 131-156. Fungal Diversity Research
     Series. Bio-exploitation of filamentous fungi. print.
     Publisher: Fungal Diversity Press Pokfulam Road, Hong Kong, Hong Kong.
     ISBN: 962-85677-2-1 (cloth).
DT   Book
LA   English

L2   ANSWER 2 OF 13  CAPLUS  COPYRIGHT 2003 ACS
AB   The invention provides methods of introducing heterologous cells into
     fish.  After introduction cells remain viable, and in some instances
     proliferate, for sufficient time to conduct a variety of analyses on the
     heterologous cells or the fish or both.  Such methods are useful for
     screening potential drugs for toxicity toward
     introduced cells or for capacity to stimulate differentiation and/or
     proliferation of introduced cells.  Such methods are also useful for
     diagnosing the presence of small quantities of cancerous cells or
     pathogens in patient tissue samples.  Such methods are also useful for
     culturing cells for subsequent use in cell or tissue engineering.  HepG2
     cells were transplanted into zebra fish embryos and studied.
AN   2000:384484  CAPLUS
DN   133:14313
TI   Methods for introducing heterologous cells into fish
IN   Serbedzija, George N.; Semino, Carlos E.; McGrath, Patricia
PA   Phylonix Pharmaceuticals, Inc., USA
SO   PCT Int. Appl., 48 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   WO 2000032822     A1    20000608      WO 1999-US28416  19991130
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
             MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
             SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     EP 1135531         A1    20010926      EP 1999-965950   19991130
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO
     US 2002061291      A1    20020523      US 1999-451489   19991130
     JP 2002531104      T2    20020924      JP 2000-585453   19991130
```

PRAI US 1998-110464P P 19981201
WO 1999-US28416 W 19991130
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 13 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AB Human papillomavirus (HPV) E6 protein forms a ternary complex with the cell-cycle regulator p53 and the E6-associated protein (E6AP) known as an E3 ubiquitin protein ligase, leading to the degradation of p53 via the ubiquitination pathway. As an attempt to employ interaction between HPV viral oncogene E6 and a cellular protein E6AP for in vitro screening system of drugs against HPV infection, we primarily investigated the E6AP-E6 binding through pull down assay and enzyme-linked immunosorbent assay (ELISA). E6AP immobilized on the resin produced specifically complexes with bacterially expressed E6 in a dose-dependent manner, as determined by immunoblot analysis. This result was collinear with that shown in ELISA, which is a useful system for mass-**screening potential drugs** with rapidity and cheapness. Screening system based on the interaction between E6AP and E6 may be a promising system in the development of drugs against cervical cancer caused by HPV infection.
AN 2000:472784 BIOSIS
DN PREV200000472784
TI Development of screening systems for drugs against human papillomavirus-associated cervical cancer: Based on E6-E6AP binding.
AU Cho, Young-Sik; Cho, Cheong-Weon; Joung, Ok; Lee, Kyung-Ae; Park, Sue-Nie; Yoon, Do-Young (1)
CS (1) Cellular Biology Lab, Korea Res. Institute of Bioscience and Biotechnology, Taejon, 305-600 South Korea
SO Antiviral Research, (September, 2000) Vol. 47, No. 3, pp. 199-206. print. ISSN: 0166-3542.
DT Article
LA English
SL English

L2 ANSWER 4 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB Assays for **screening potential drugs** or agents that can interact and potentially bind to cation channel proteins, and potentially have uses in treating conditions related to the function of cation channel proteins is provided, along with prokaryotic cation channel proteins mutated to mimic eukaryotic cation channels, which can then be used in assays of the present invention.
AN 1999:614249 CAPLUS
DN 131:252536
TI Assays for screening compounds which interact with cation channel proteins, mutant prokaryotic cation channel proteins, and uses thereof
IN MacKinnon, Roderick
PA The Rockefeller University, USA
SO PCT Int. Appl., 165 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9947923	A2	19990923	WO 1999-US6307	19990322
WO 9947923	A3	20021003		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2323725 AA 19990923 CA 1999-2323725 19990322
AU 9931988 A1 19991011 AU 1999-31988 19990322
EP 1062508 A1 20001227 EP 1999-914058 19990322
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI US 1998-45529 A 19980320
US 1998-54347 A2 19980402
WO 1999-US6307 W 19990322

L2 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB The principal agent in the etiol. of cervical cancer, i.e., human papillomavirus (HPV) type 16, encodes three oncoproteins, E5, E6, and E7. Structural and mutational studies have identified two potential zinc-finger domains as crit. for E6 protein function. We investigated several assays to identify and characterize compds. that interfere with the binding of zinc to E6. Thirty-six compds. were selected on the basis of their structure, which would facilitate their participation in sulfhydryl residue-specific redox reactions, and were tested for their ability to release zinc from E6 protein. The zinc-ejecting compds. were then tested for their ability to inhibit E6 binding to E6-assocd. protein (E6AP) and E6-binding protein (E6BP), two coactivators of E6-mediated cellular transformation. The binding of E6 to E6BP and E6AP was measured by use of surface plasmon resonance (a technique that monitors mol. interactions by measuring changes in refractive index) and by use of in vitro translation assays. The compds. were also tested for their effects on the viability of HPV-contg. cell lines. Nine of the 36 tested compds. ejected zinc from E6. Two of the nine compds. inhibited the interaction of E6 with E6AP and E6BP, and one of these two, 4,4'-dithiodimorpholine, selectively inhibited cell viability and induced higher levels of p53 protein (assocd. with the induction of apoptosis [programmed cell death]) in tumorigenic HPV-contg. cells. We have described assay systems to identify compds., such as 4,4'-dithiodimorpholine, that can potentially interfere with the biol. and pathol. of HPV. These assay systems may be useful in the development of drugs against cervical cancer, genital warts, and asymptomatic infections by genital HPVs.
AN 1999:507293 CAPLUS
DN 132:87659
TI Potential drugs against cervical cancer: zinc-ejecting inhibitors of the human papillomavirus type 16 E6 oncoprotein
AU Beerheide, Walter; Bernard, Hans-Ulrich; Tan, Yee-Joo; Ganesan, Arasu; Rice, William G.; Ting, Anthony E.
CS Screening for Novel Inhibitors Laboratory, Institute of Molecular and Cell Biology, Singapore, 117609, Singapore
SO Journal of the National Cancer Institute (1999), 91(14), 1211-1220
CODEN: JNCIEQ; ISSN: 0027-8874
PB Oxford University Press
DT Journal
LA English
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 13 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AB The analytical challenges for biomarkers used for **screening potential drugs** are growing as well as the demands for automation and sample throughput. One way of attacking these problems is to combine specific properties from different technologies into one functional analytical method. In early phases of synthetic drug screening the effect of several substances needs to be monitored in a minimum of time. In later phases, mechanistic and more detailed information about the mode of action is required for which more selective and sensitive methods

are needed. In the animal models used, the effect of the candidate drug on certain endogenous compounds responsible for progress of the disease is important to establish but also the effect on other biomarkers which production is either stimulated or suppressed as a consequence of the action of the potential drug. The biomarkers and their important metabolites have to be identified and subsequently determined at clinically effective drug concentrations. Here we present an integrated approach which describes the different requirements for the analysis of leukotrienes in several phases of drug research. Key parts of the analytical methodology are the on-line coupling of liquid chromatography to continuous-flow fluoro-immuno ligand assays and efficient sample handling. The technology can be applied to early phase drug developments where fast screening of biological samples are of importance and can be achieved by total immunoaffinity responses. Later in the development phase when metabolic identification is outlined, qualitative and quantitative determinations are achieved using the fully integrated and automated flow system.

AN 1997:397256 BIOSIS
DN PREV199799696459
TI Biomarker monitoring in pharmaceutical research: Measurement of leukotrienes and their metabolites using on-line liquid chromatography-flow immuno ligand assay.
AU Oosterkamp, Aaike J.; Irth, Hubertus; Marko-Varga, Gyorgy; Heintz, Lena; Kjellstrom, Sven; Alkner, Ulf (1)
CS (1) Astra Draco AB, Bioanalytical Chem., P.O. Box 34, S-221 00 Lund Sweden
SO Journal of Clinical Ligand Assay, (1997) Vol. 20, No. 1, pp. 40-48. ISSN: 1081-1672.
DT Article
LA English

L2 ANSWER 7 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB A review with 14 refs. With the help of so-called combinatorial chem. (CC), the rapid and automated, and, if necessary, simultaneous synthesis of many thousands of compds. is now feasible. Within a very short time, the researcher may have libraries of compds. at his disposal. Esp. the pharmaceutical industry has discovered the power of this method for **screening potential drugs**. Synthesis of compds. (e.g. benzodiazepines) on resin supports, synthesis of a mixt. of substances with a cluster of properties, and combination of CC with rational (structure-based) drug design.

AN 1995:487567 CAPLUS
DN 123:208574
TI Combinatorial chemistry. Mass production of synthesis compounds
AU Hermkens, Pedro; Ottenheijm, Harry; de Ridder, Hans
CS Organon Scientific Development Group, Neth.
SO Chemisch Magazine (Rijswijk, Netherlands) (1995), (1), 19-22 CODEN: CMAGDR; ISSN: 0167-2746
PB Stam Tijdschriften bv
DT Journal; General Review
LA Dutch

L2 ANSWER 8 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB The cell line 81C, sarcoma-pos./leukemia-neg., was used to successfully detect the antiviral activity of 3'-azido-3'-deoxythymidine (AZT) and 2',3'-dideoxycytidine against feline leukemia virus (FLV), a model retrovirus. 2',3'-Dideoxyinosine and 2',3'-dideoxyadenosine were less effective. The in vivo antiviral activity of AZT against FLV infection of specific pathogen-free cats is reviewed. Both the in vitro and in vivo systems should be useful for **screening potential drugs** for AIDS therapy.

AN 1989:204955 CAPLUS
DN 110:204955
TI Testing of nucleoside analogs in cats infected with feline leukemia virus: a model

AU Tavares, Luis; Roneker, Carol; Postie, Lori; De Noronha, Fernando
CS New York State Coll. Vet. Med., Cornell Univ., Ithaca, NY, 14853, USA
SO Intervirology (1989), 30(Suppl. 1), 26-35
CODEN: IVRYAK; ISSN: 0300-5526
DT Journal
LA English

L2 ANSWER 9 OF 13 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
AB Administration of p,p'-DDT to rats produced myoclonus, but unlike previous studies in mice, this was not decreased by administration of clonazepam. Precursors of 5-hydroxytryptamine (5-HT) (L-tryptophan and L-5-HTP) reduced the intensity of myoxlonus, but the 5-HT agonists, quipazine and Org 6582 did not. Antagonists of 5-HT (methergoline, methysergide and cinanserin) did not potentiate the myoclonus induced by p,p'-DDT. Drugs altering the function of dopamine and noradrenaline (apomorphine, clonidine or phenoxybenzamine) also had no effect on this myoclonus. Administration of monoamine oxidase inhibitors (MAOI; pargyline, nialamide and tranylcypromine) markedly attenuated the myoclonus, an effect that could not be attributed to an action on any 1 monoamine system. No observable changes in cerebral biochemical parameters of 5-HT occurred at the onset of myoclonus, although tryptophan and 5-hydroxyindoleacetic acid (5-HIAA) in brain were increased following periods of prolonged myoclonus. Electrophysiological analysis of the myoclonus in the rat induced by p,p'-DDT revealed changes in EEG and EMG activity which suggested an origin for the myoclonus in the brainstem. Although this was similar to electrophysiological findings in some human patients with post-anoxic action myoclonus, the pharmacological studies suggest that the myoclonus induced by p,p'-DDT in the rat is not a suitable model for **screening potential drugs** to be used in the treatment of this disorder.
AN 1985:373343 BIOSIS
DN BA80:43335
TI MYOCLONUS IN THE RAT INDUCED BY P P' DDT AND THE ROLE OF ALTERED MONOAMINE FUNCTION.
AU PRATT J A; ROTHWELL J; JENNER P; MARSDEN C D
CS KING'S COLL. HOSP. MED. SCH., DENMARK HILL, LONDON SE5, ENGLAND.
SO NEUROPHARMACOLOGY, (1985) 24 (5), 361-374.
CODEN: NEPHBW. ISSN: 0028-3908.
FS BA; OLD
LA English

L2 ANSWER 10 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB 108ML15 neuroblastoma .times. glioma hybrid cells were shown to possess a high-affinity [3H]-labeled imipramine (I) [50-49-7]-binding site (Kd = 210 nM, Bmax = 0.22 nmol/5 .times. 105 cells) and a 2nd site of lower affinity (Kd 16.5 .mu.M, Bmax = 3.81 nmol/5 .times. 105 cells). Displacement studies on the high-affinity binding site showed that the antidepressant drugs studied displaced I to different extents. The mean clin. efficacy of the drugs correlated well with their ability to displace I. As neither 5-hydroxytryptamine nor noradrenaline at concns. of <1 mM was capable of displacing I, it is unlikely that the binding sites are related to the receptors for these ligands. The binding sites for I present on 108ML15 hybrid cells were closely related to or identical with the central nervous system receptors that are the pharmacol. significant sites of action of tricyclic antidepressants in depressive illness. These cells should prove to be excellent models for the elucidation of the mode of action of these drugs and for **screening potential drugs** of this type.
AN 1984:61625 CAPLUS
DN 100:61625
TI 108CC15 neuroblastoma .times. glioma hybrid cells possess pharmacologically relevant imipramine-t binding sites
AU Snell, Penelope H.; Snell, Christopher R.

CS MRC Neuroendocrinol. Unit, Newcastle Gen. Hosp., Newcastle upon Tyne, NE4 6BE, UK
SO Biochemical Society Transactions (1983), 11(2), 209-10
CODEN: BCSTB5; ISSN: 0300-5127
DT Journal
LA English

L2 ANSWER 11 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB The use of the rat is proposed for inexpensively and quickly **screening potential drugs** for toxicity. The approach includes a clin. evaluation and clin.-chem. and hematol. tests, and the data are collated with a simple computer program. Over a 2-yr period, the rat toxicity screen disclosed most toxicity eventually uncovered by more conventional, and time-consuming, methods. A tabulation of abnormalities disclosed by this method is given. Bioavailability data can also be derived from this procedure, which expends only .apprx.1.5 g of compd.
AN 1979:550956 CAPLUS
DN 91:150956
TI The rat toxicity screen
AU Fowler, J. S. L.; Brown, J. S.; Bell, H. A.
CS Pharm. Div., ICI Ltd., Macclesfield/Cheshire, UK
SO Pharmacology & Therapeutics (1979), 5(1-3), 461-6
CODEN: PHTHDT; ISSN: 0163-7258
DT Journal
LA English

L2 ANSWER 12 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB A review with 19 refs. of normal and pathol. bronchial mucosa biochemistry, drugs used in treating bronchial secretion disorders, and methods used for studying bronchial secretions and **screening potential drugs**.
AN 1972:456256 CAPLUS
DN 77:56256
TI Modifiers of bronchial secretions
AU Quevauviller, Andre; Garcet, Suzanne; Huyen Vu Ngoc
CS Fr.
SO Produits & Problemes Pharmaceutiques (1972), 27(4), 267-80
CODEN: PPRPAS; ISSN: 0032-9959
DT Journal; General Review
LA French

L2 ANSWER 13 OF 13 CAPLUS COPYRIGHT 2003 ACS
AB A review of recent advances in non-steroidal antiinflammatory drugs. Synthesis and bioactivity of antiinflammatory salicylic acids and salicylamides, arylacetic acids (particularly indolyl), anthranilic acid, and phenylbutazone analogs were discussed. The physiolog. and biochem. causes of inflammation were outlined. Techniques were listed for generating exptl. inflammation in lab. animals suitable for **screening potential drugs**. 36 refs.
AN 1971:405747 CAPLUS
DN 75:5747
TI Newer antiinflammatory drugs
AU Unterhalt, Bernard
CS Landesgruppe Bremen, Dtsch. Pharm. Ges., Marburg, Fed. Rep. Ger.
SO Deutsche Apotheker Zeitung (1971), 111(8), 263-9
CODEN: DAZEA2; ISSN: 0011-9857
DT Journal; General Review
LA German

=> s detection of virulence
3 FILES SEARCHED...
L3 210 DETECTION OF VIRULENCE

```
=> s l1 and tatB
L4            0 L1 AND TATB

=> dup rem l3
PROCESSING COMPLETED FOR L3
L5            89 DUP REM L3 (121 DUPLICATES REMOVED)

=> s l5 and tatb
L6            0 L5 AND TATB

=> s tatB
L7          941 TATB

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8           760 DUP REM L7 (181 DUPLICATES REMOVED)

=> s l8 and operon
L9            5 L8 AND OPERON

=> d kwic, abs, bib

L9   ANSWER 1 OF 5  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB.  . . coli twin arginine translocation (Tat) system mediates
     Sec-independent export of protein precursors bearing twin arginine signal
     peptides. The genes tatA, tatB, tatC and tatE code for integral
     membrane proteins that are components of the Tat pathway. Cells
     co-overexpressing tatABCDE show an increased rate of export of a signal
     peptide-defective Tat precursor protein and a complex containing the TatA
     and TatB proteins can be purified from the membranes of such
     cells. The purified TatAB complex has an apparent molecular mass of. . .
     measured by gel permeation chromatography and, like the membranes of
     wild-type cells, contains a large molar excess of TatA over TatB
     . Negative stain electron microscopy of the complex reveals cylindrical
     structures that may correspond to the Tat protein transport channel.
IT   . . .
        and Molecular Biophysics); Membranes (Cell Biology)
IT   Parts, Structures, & Systems of Organisms
        cell; membrane
IT   Chemicals & Biochemicals
        TatA; TatB; TatC; protein precursor: twin arginine signal
        peptide; tatABCDE operon
GEN  Escherichia coli tatA gene (Enterobacteriaceae); Escherichia coli
     tatB gene (Enterobacteriaceae); Escherichia coli tatC gene
     (Enterobacteriaceae); Escherichia coli tatE gene (Enterobacteriaceae)
AB   The Escherichia coli twin arginine translocation (Tat) system mediates
     Sec-independent export of protein precursors bearing twin arginine signal
     peptides. The genes tatA, tatB, tatC and tatE code for integral
     membrane proteins that are components of the Tat pathway. Cells
     co-overexpressing tatABCDE show an increased rate of export of a signal
     peptide-defective Tat precursor protein and a complex containing the TatA
     and TatB proteins can be purified from the membranes of such
     cells. The purified TatAB complex has an apparent molecular mass of 600
     kDa as measured by gel permeation chromatography and, like the membranes
     of wild-type cells, contains a large molar excess of TatA over
     TatB. Negative stain electron microscopy of the complex reveals
     cylindrical structures that may correspond to the Tat protein transport
     channel.
AN   2001:344736  BIOSIS
DN   PREV200100344736
TI   Purified components of the Escherichia coli Tat protein transport system
     form a double-layered ring structure.
AU   Sargent, Frank; Gohlke, Ulrich; de Leeuw, Erik; Stanley, Nicola R.;
```

Palmer, Tracy; Saibil, Helen R.; Berks, Ben C. (1)
CS (1) School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ: b.berks@uea.ac.uk UK
SO European Journal of Biochemistry, (June, 2001) Vol. 268, No. 12, pp. 3361-3367. print.
ISSN: 0014-2956.
DT Article
LA English
SL English

=> d kwic, abs, bib 2-5

L9 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB . . Sec-independent export of protein precursors bearing twin arginine signal peptides. Genes known to be involved in this process include tatA, **tatB**, and tatC that form an **operon** with a fourth gene, tatD. The tatD gene product has two homologues in E. coli coded by the unlinked ycfH. . . cytoplasmic protein. TatD binds to immobilized Ni2+ or Zn2+ affinity columns and exhibits magnesium-dependent DNase activity. Features of the tatA **operon** that may control TatD expression are discussed.
IT . . .
of Organisms
cytoplasm
IT Chemicals & Biochemicals
DNase; Sec; TatD: cytoplasmic protein; arginine; Escherichia coli tatA gene (Enterobacteriaceae); Escherichia coli **tatB** gene (Enterobacteriaceae); Escherichia coli tatC gene (Enterobacteriaceae); Escherichia coli tatD gene (Enterobacteriaceae); Escherichia coli ycfH gene (Enterobacteriaceae); Escherichia coli yjjV. . .
AB The Escherichia coli Tat system mediates Sec-independent export of protein precursors bearing twin arginine signal peptides. Genes known to be involved in this process include tatA, **tatB**, and tatC that form an **operon** with a fourth gene, tatD. The tatD gene product has two homologues in E. coli coded by the unlinked ycfH and yjjV genes. An E. coli strain with in-frame chromosomal deletions in all three of tatD, ycfH, and yjjV exhibits no significant defect in the cellular location of five cofactor-containing enzymes that are synthesized with twin arginine signal peptides. Neither these mutations nor overproduction of the TatD protein cause any discernible effect on the export kinetics of an additional E. coli Tat pathway substrate. It is concluded that proteins of the TatD family have no obligate involvement in protein export by the Tat system. TatD is shown to be a cytoplasmic protein. TatD binds to immobilized Ni2+ or Zn2+ affinity columns and exhibits magnesium-dependent DNase activity. Features of the tatA **operon** that may control TatD expression are discussed.
AN 2000:309151 BIOSIS
DN PREV200000309151
TI TatD is a cytoplasmic protein with DNase activity: No requirement for TatD family proteins in Sec-independent protein export.
AU Wexler, Margaret; Sargent, Frank; Jack, Rachael L.; Stanley, Nicola R.; Bogsch, Erik G.; Robinson, Colin; Berks, Ben C. (1); Palmer, Tracy
CS (1) School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ UK
SO Journal of Biological Chemistry, (June 2, 2000) Vol. 275, No. 22, pp. 16717-16722. print.
ISSN: 0021-9258.
DT Article
LA English
SL English

L9 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB . . translocation of folded proteins. One of the two HCF106 homologues

is encoded by the first gene of a four cistron **operon**, tatABCD, and the second by an unlinked gene, tatE. A mutation previously assigned to the hcf106 homologue encoded at the tatABCD locus, mttA, lies instead in the **tatB** gene.

IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Chemicals & Biochemicals
mttA; tatABCD; **tatB** gene; tatE gene; HCF106 protein

AB We describe the identification of two Escherichia coli genes required for the export of cofactor-containing periplasmic proteins, synthesized with signal peptides containing a twin arginine motif. Both gene products are homologous to the maize HCF106 protein required for the translocation of a subset of lumenal proteins across the thylakoid membrane. Disruption of either gene affects the export of a range of such proteins, and a complete block is observed when both genes are inactivated. The Sec protein export pathway was unaffected, indicating the involvement of the gene products in a novel export system. The accumulation of active cofactor-containing proteins in the cytoplasm of the mutant strains suggests a role for the gene products in the translocation of folded proteins. One of the two HCF106 homologues is encoded by the first gene of a four cistron **operon**, tatABCD, and the second by an unlinked gene, tatE. A mutation previously assigned to the hcf106 homologue encoded at the tatABCD locus, mttA, lies instead in the **tatB** gene.

AN 1998:361626 BIOSIS

DN PREV199800361626

TI Overlapping functions of components of a bacterial Sec-independent protein export pathway.

AU Sargent, Frank; Bogsch, Erik G.; Stanley, Nicola R.; Wexler, Margaret; Robinson, Colin; Berks, Ben C.; Palmer, Tracy (1)

CS (1) Nitrogen Fixation Lab., John Innes Centre, Colney, Norwich NR4 7UH UK

SO EMBO (European Molecular Biology Organization) Journal, (July 1, 1998) Vol. 17, No. 13, pp. 3640-3650.
ISSN: 0261-4189.

DT Article

LA English

L9 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2003 ACS

AB . . . E. coli Tat-app., whereas the folded mature part of GFOR is compatible with Tat-dependent translocation in E. coli. The tatABC **operon** of Z. mobilis was cloned. The single Tat proteins TatA, **TatB** and TatC of Z. mobilis are functional in E. coli and at least one of these proteins is involved in. . . grow under certain anaerobic growth conditions. In a first test of the screening assay, several mutants in the already known tatABC-**operon** were selectively isolated.

ST Tat protein translocation pathway Escherichia Zymomonas; sequence tatABC **operon** protein Zymomonas

IT DNA sequences
(of tatABC **operon** of Zymomonas mobilis)

IT Protein sequences
(of tatABC **operon** proteins of Zymomonas mobilis)

IT **Operon**
(tatABC; characterization of Tat-dependent protein translocation pathway in Gram-neg. bacteria)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(**tatB**; characterization of Tat-dependent protein translocation pathway in Gram-neg. bacteria)

IT 388636-81-5, Protein (Zymomonas mobilis gene tatA) 388636-82-6, Protein (Zymomonas mobilis gene **tatB**)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; characterization of Tat-dependent protein

translocation pathway in Gram-neg. bacteria)

AB Tat-dependent protein translocation was investigated in Escherichia coli and Zymomonas mobilis with regard to species specific differences. E. coli is unable to export the authentic Tat-substrate glucose-fructose oxidoreductase (GFOR) of Z. mobilis. The replacement of the Z. mobilis GFOR signal peptide by the E. coli Tat signal peptide of the trimethylamine NO (TMAO) reductase (TorA) leads to an efficient, strictly Tat-dependent export of the mature GFOR in E. coli. This result shows that the GFOR signal sequence is not recognized by the E. coli Tat-app., whereas the folded mature part of GFOR is compatible with Tat-dependent translocation in E. coli. The tatABC **operon** of Z. mobilis was cloned. The single Tat proteins TatA, **TatB** and TatC of Z. mobilis are functional in E. coli and at least one of these proteins is involved in the specific recognition of the GFOR signal sequence (Tat signal peptide receptor). Therefore, a specific recognition event between Tat substrate and Tat receptor takes place that goes beyond the recognition of the conserved general features found in all Tat signal peptides. The species specificity of signal sequence recognition in the Tat pathway is in marked contrast to the situation that is known to exist for the Sec pathway. In E. coli, only four different components of the Tat pathway are known so far. Therefore, a screening assay that is suitable for the identification of so far unknown tat-genes was established. In this assay, a TorA-MalE fusion protein was proved to be an ideal reporter protein for the Tat-pathway. Due to a strong Sec avoidance motif in the C-region of the TorA signal sequence, export of the fusion protein is strictly Tat-dependent. Export is essential for maltose metab. in a malE-neg. E. coli strain and easy to detect on maltose-contg. indicator plates. After mutagenesis of an E. coli Tat wild type strain, mutants which are unable to metabolize maltose due to a mutation in genes of the Tat pathway or maltose metab., were selected from the indicator plates. The tat-mutants were identified by means of their inability to grow under certain anaerobic growth conditions. In a first test of the screening assay, several mutants in the already known tatABC-**operon** were selectively isolated.

AN 2001:912743 CAPLUS

DN 136:97050

TI Characterization of the Tat-dependent protein translocation pathway in Gram-negative bacteria

AU Blaudeck, Anke Natascha

CS Germany

SO Berichte des Forschungszentrums Juelich (2001), Juel-3872, i-ix, 1-97, 99-107
CODEN: FJBEE5; ISSN: 0366-0885

DT Report

LA German

RE.CNT 94 THERE ARE 94 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2003 ACS

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene **SMc00466**, transmembrane protein sequence homolog; anal. of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene SMc00904; anal. of **the** chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021)

AB Sinorhizobium meliloti is an .alpha.-proteobacterium that forms agronomically important N2-fixing root nodules in legumes. We report here the complete sequence of the largest constituent of its genome, a 62.7% GC-rich 3654,135-bp circular chromosome. Annotation allowed assignment of

a function to 59% of the 3341 predicted protein-coding ORFs, the rest exhibiting partial, weak, or no similarity with any known sequence. Unexpectedly, the level of reiteration within this replicon is low, with only two genes duplicated with more than 90% nucleotide sequence identity, transposon elements accounting for 2.2% of the sequence, and a few hundred short repeated palindromic motifs (RIME1, RIME2, and C) widespread over the chromosome. Three regions with a significantly lower GC content are most likely of external origin. Detailed annotation revealed that this replicon contains all housekeeping genes except two essential genes that are located on pSymB. Amino acid/peptide transport and degrdn. and sugar metab. appear as two major features of the S. meliloti chromosome. The presence in this replicon of a large no. of nucleotide cyclases with a peculiar structure, as well as of genes homologous to virulence determinants of animal and plant pathogens, opens perspectives in the study of this bacterium both as a free-living soil microorganism and as a plant symbiont.

AN 2001:634531 CAPLUS
DN 136:258038
TI Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021
AU Capela, Delphine; Barloy-Hubler, Frederique; Gouzy, Jerome; Bothe, Gordana; Ampe, Frederic; Batut, Jacques; Boistard, Pierre; Becker, Anke; Boutry, Marc; Cadieu, Edouard; Dreano, Stephane; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre; Kahn, Daniel; Kiss, Erno; Lelaure, Valerie; Masuy, David; Pohl, Thomas; Portetelle, Daniel; Puhler, Alfred; Purnelle, Benedicte; Ramsperger, Ulf; Renard, Clotilde; Thebault, Patricia; Vandenbol, Micheline; Weidner, Stefan; Galibert, Francis
CS Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, Unite Mixte de Recherche (UMR) 215 Centre National de la Recherche Scientifique (CNRS), Institut National de la Recherche Agronomique, Chemin, Tolosan, F-31326, Fr.
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(17), 9877-9882
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s l2 and operon
L10 1 L2 AND OPERON

=> d kwic, abs, bib

L10 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS
AB Assays for **screening potential drugs** or agents that can interact and potentially bind to cation channel proteins, and potentially have uses in treating conditions related. . .
IT **Operon**
(lac; mutant prokaryotic cation channel proteins and assays for screening compds. which interact with cation channel proteins)
IT **Operon**
(trp; mutant prokaryotic cation channel proteins and assays for screening compds. which interact with cation channel proteins)
AB Assays for **screening potential drugs** or agents that can interact and potentially bind to cation channel proteins, and potentially have uses in treating conditions related to the function of cation channel proteins is provided, along with prokaryotic cation channel proteins mutated to mimic eukaryotic cation channels, which can then be used in assays of the present invention.
AN 1999:614249 CAPLUS
DN 131:252536

TI Assays for screening compounds which interact with cation channel proteins, mutant prokaryotic cation channel proteins, and uses thereof
IN MacKinnon, Roderick
PA The Rockefeller University, USA
SO PCT Int. Appl., 165 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9947923	A2	19990923	WO 1999-US6307	19990322
	WO 9947923	A3	20021003		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2323725	AA	19990923	CA 1999-2323725	19990322
	AU 9931988	A1	19991011	AU 1999-31988	19990322
	EP 1062508	A1	20001227	EP 1999-914058	19990322
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	US 1998-45529	A	19980320		
	US 1998-54347	A2	19980402		
	WO 1999-US6307	W	19990322		

=> s l7 and operon
L11 18 L7 AND OPERON

=> d abis, bib
'ABIS' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):s abs, bib
'S' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d abs, bib
'D' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):.

L11 ANSWER 1 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2001:344736 BIOSIS
DN PREV200100344736
TI Purified components of the Escherichia coli Tat protein transport system form a double-layered ring structure.
AU Sargent, Frank; Gohlke, Ulrich; de Leeuw, Erik; Stanley, Nicola R.; Palmer, Tracy; Saibil, Helen R.; Berks, Ben C. (1)
CS (1) School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ: b.berks@uea.ac.uk UK

SO European Journal of Biochemistry, (June, 2001) Vol. 268, No. 12, pp. 3361-3367. print.
ISSN: 0014-2956.
DT Article
LA English
SL English

=> d abs, bib 10-18

L11 ANSWER 10 OF 18 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
AB We describe the identification of two Escherichia coli genes required for the export of cofactor-containing periplasmic proteins, synthesized with signal peptides containing a twin arginine motif. Both gene products are homologous to the maize HCF106 protein required for the translocation of a subset of lumenal proteins across the thylakoid membrane. Disruption of either gene affects the export of a range of such proteins, and a complete block is observed when both genes are inactivated. The Sec protein export pathway was unaffected, indicating the involvement of the gene products in a novel export system. The accumulation of active cofactor-containing proteins in the cytoplasm of the mutant strains suggests a role for the gene products in the translocation of folded proteins. One of the two HCF106 homologues is encoded by the first gene of a four cistron **operon**, tatABCD, and the second by an unlinked gene, tatE. A mutation previously assigned to the hcf106 homologue encoded at the tatABCD locus, mttA, lies instead in the **tatB** gene.
AN 1998237566 EMBASE
TI Overlapping functions of components of a bacterial Sec-independent protein export pathway.
AU Sargent F.; Bogsch E.G.; Stanley N.R.; Wexler M.; Robinson C.; Berks B.C.; Palmer T.
CS T. Palmer, Nitrogen Fixation Laboratory, John Innes Centre, Norwich NR4 7UH, United Kingdom. PALMER@BBRSC.AC.UK
SO EMBO Journal, (1 Jul 1998) 17/13 (3640-3650).
Refs: 63
ISSN: 0261-4189 CODEN: EMJODG
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
029 Clinical Biochemistry
LA English
SL English

L11 ANSWER 11 OF 18 CAPLUS COPYRIGHT 2003 ACS
AB Tat-dependent protein translocation was investigated in Escherichia coli and Zymomonas mobilis with regard to species specific differences. E. coli is unable to export the authentic Tat-substrate glucose-fructose oxidoreductase (GFOR) of Z. mobilis. The replacement of the Z. mobilis GFOR signal peptide by the E. coli Tat signal peptide of the trimethylamine NO (TMAO) reductase (TorA) leads to an efficient, strictly Tat-dependent export of the mature GFOR in E. coli. This result shows that the GFOR signal sequence is not recognized by the E. coli Tat-app., whereas the folded mature part of GFOR is compatible with Tat-dependent translocation in E. coli. The tatABC **operon** of Z. mobilis was cloned. The single Tat proteins TatA, **TatB** and TatC of Z. mobilis are functional in E. coli and at least one of these proteins is involved in the specific recognition of the GFOR signal sequence (Tat signal peptide receptor). Therefore, a specific recognition event between Tat substrate and Tat receptor takes place that goes beyond the recognition of the conserved general features found in all Tat signal peptides. The species specificity of signal sequence recognition in the Tat pathway is in marked contrast to the situation that is known to exist for the Sec pathway. In E. coli, only four different components of the Tat pathway are known so far. Therefore, a screening assay that is

suitable for the identification of so far unknown tat-genes was established. In this assay, a TorA-MalE fusion protein was proved to be an ideal reporter protein for the Tat-pathway. Due to a strong Sec avoidance motif in the C-region of the TorA signal sequence, export of the fusion protein is strictly Tat-dependent. Export is essential for maltose metab. in a malE-neg. E. coli strain and easy to detect on maltose-contg. indicator plates. After mutagenesis of an E. coli Tat wild type strain, mutants which are unable to metabolize maltose due to a mutation in genes of the Tat pathway or maltose metab., were selected from the indicator plates. The tat-mutants were identified by means of their inability to grow under certain anaerobic growth conditions. In a first test of the screening assay, several mutants in the already known tatABC-**operon** were selectively isolated.

AN 2001:912743 CAPLUS
DN 136:97050
TI Characterization of the Tat-dependent protein translocation pathway in Gram-negative bacteria
AU Blaudeck, Anke Natascha
CS Germany
SO Berichte des Forschungszentrums Juelich (2001), Juel-3872, i-ix, 1-97, 99-107
CODEN: FJBEE5; ISSN: 0366-0885
DT Report
LA German
RE.CNT 94 THERE ARE 94 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2003 ACS
AB Sinorhizobium meliloti is an .alpha.-proteobacterium that forms agronomically important N2-fixing root nodules in legumes. We report here the complete sequence of the largest constituent of its genome, a 62.7% GC-rich 3654,135-bp circular chromosome. Annotation allowed assignment of a function to 59% of the 3341 predicted protein-coding ORFs, the rest exhibiting partial, weak, or no similarity with any known sequence. Unexpectedly, the level of reiteration within this replicon is low, with only two genes duplicated with more than 90% nucleotide sequence identity, transposon elements accounting for 2.2% of the sequence, and a few hundred short repeated palindromic motifs (RIME1, RIME2, and C) widespread over the chromosome. Three regions with a significantly lower GC content are most likely of external origin. Detailed annotation revealed that this replicon contains all housekeeping genes except two essential genes that are located on pSymB. Amino acid/peptide transport and degrdn. and sugar metab. appear as two major features of the S. meliloti chromosome. The presence in this replicon of a large no. of nucleotide cyclases with a peculiar structure, as well as of genes homologous to virulence determinants of animal and plant pathogens, opens perspectives in the study of this bacterium both as a free-living soil microorganism and as a plant symbiont.
AN 2001:634531 CAPLUS
DN 136:258038
TI Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021
AU Capela, Delphine; Barloy-Hubler, Frederique; Gouzy, Jerome; Bothe, Gordana; Ampe, Frederic; Batut, Jacques; Boistard, Pierre; Becker, Anke; Boutry, Marc; Cadieu, Edouard; Dreano, Stephane; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre; Kahn, Daniel; Kiss, Erno; Lelaure, Valerie; Masuy, David; Pohl, Thomas; Portetelle, Daniel; Puhler, Alfred; Purnelle, Benedicte; Ramsperger, Ulf; Renard, Clotilde; Thebault, Patricia; Vandenbol, Micheline; Weidner, Stefan; Galibert, Francis
CS Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, Unite Mixte de Recherche (UMR) 215 Centre National de la Recherche Scientifique (CNRS), Institut National de la Recherche Agronomique, Chemin, Tolosan, F-31326, Fr.
SO Proceedings of the National Academy of Sciences of the United States of

America (2001), 98(17), 9877-9882
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 13 OF 18 CAPLUS COPYRIGHT 2003 ACS
AB The transcription start sites for the tatABCD and tatE loci, encoding components of the Tat (twin-arginine translocase) protein export pathway, have been identified. Expression studies indicate that the tatABCD and tatE transcription units are expressed constitutively. Translational fusion expts. suggest that TatA is synthesized at a much higher level than the other Tat proteins.
AN 2001:137916 CAPLUS
DN 135:222204
TI Constitutive expression of Escherichia coli tat genes indicates an important role for the twin-arginine translocase during aerobic and anaerobic growth
AU Jack, Rachael L.; Sargent, Frank; Berks, Ben C.; Sawers, Gary; Palmer, Tracy
CS Centre for Metalloprotein Spectroscopy and Biology, School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ, UK
SO Journal of Bacteriology (2001), 183(5), 1801-1804
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 14 OF 18 CAPLUS COPYRIGHT 2003 ACS
AB The Escherichia coli Tat system mediates Sec-independent export of protein precursors bearing twin arginine signal peptides. Genes known to be involved in this process include tatA, **tatB**, and tatC that form an **operon** with a fourth gene, tatD. The tatD gene product has two homologues in E. coli coded by the unlinked ycfH and yjjV genes. An E. coli strain with in-frame chromosomal deletions in all three of tatD, ycfH, and yjjV exhibits no significant defect in the cellular location of five cofactor-contg. enzymes that are synthesized with twin arginine signal peptides. Neither these mutations nor overprodn. of the TatD protein cause any discernible effect on the export kinetics of an addnl. E. coli Tat pathway substrate. It is concluded that proteins of the TatD family have no obligate involvement in protein export by the Tat system. TatD is shown to be a cytoplasmic protein. TatD binds to immobilized Ni2+ or Zn2+ affinity columns and exhibits magnesium-dependent DNase activity. Features of the tatA **operon** that may control TatD expression are discussed.
AN 2000:394495 CAPLUS
DN 133:132237
TI TatD is a cytoplasmic protein with DNase activity. No requirement for TatD family proteins in Sec-independent protein export
AU Wexler, Margaret; Sargent, Frank; Jack, Rachael L.; Stanley, Nicola R.; Bogsch, Erik G.; Robinson, Colin; Berks, Ben C.; Palmer, Tracy
CS Centre for Metalloprotein Spectroscopy and Biology, School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ, UK
SO Journal of Biological Chemistry (2000), 275(22), 16717-16722
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 15 OF 18 CAPLUS COPYRIGHT 2003 ACS
AB The identification of 2 Escherichia coli genes required for the export of cofactor-contg. periplasmic proteins, synthesized with signal peptides contg. a twin arginine motif, is described. Both gene products are homologous to the maize HCF106 protein required for the translocation of a subset of lumenal proteins across the thylakoid membrane. Disruption of either gene affects the export of a range of such proteins, and a complete block is obsd. when both genes are inactivated. The Sec protein export pathway was unaffected, indicating the involvement of the gene products in a novel export system. The accumulation of active cofactor-contg. proteins in the cytoplasm of the mutant strains suggests a role for the gene products in the translocation of folded proteins. One of the 2 HCF106 homologs is encoded by the 1st gene of a 4-cistron **operon**, tatABCD, and the 2nd by an unlinked gene, tatE. A mutation previously assigned to the hcf106 homolog encoded at the tatABCD locus, mttA, lies instead in the **tatB** gene.
AN 1998:470053 CAPLUS
DN 129:186541
TI Overlapping functions of components of a bacterial Sec-independent protein export pathway
AU Sargent, Frank; Bogsch, Erik G.; Stanley, Nicola R.; Wexler, Margaret; Robinson, Colin; Berks, Ben C.; Palmer, Tracy
CS Nitrogen Fixation Laboratory, John Innes Centre, Norwich, NR4 7UH, UK
SO EMBO Journal (1998), 17(13), 3640-3650
CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 16 OF 18 MEDLINE
AB In Escherichia coli, a subset of periplasmic proteins is exported via the twin-arginine translocation (Tat) pathway. In the present study, we have purified the Tat complex from E. coli, and we show that it contains only TatA, **TatB**, and TatC. Within the purified complex, **TatB** and TatC are present in a strict 1:1 ratio, suggesting a functional association. This has been confirmed by expression of a translational fusion between **TatB** and TatC. This Tat(BC) chimera supports efficient Tat-dependent export, indicating that **TatB** and TatC act as a unit in both structural and functional terms. The purified Tat complex contains varying levels of TatA, suggesting a gradual loss during isolation and a looser association. The molecular mass of the complex is approximately 600 kDa, demonstrating the presence of multiple copies of TatA, B, and C. Co-immunoprecipitation experiments show that TatC is required for the interaction of TatA with **TatB**, suggesting that TatA may interact with the complex via binding to TatC.
AN 2001316464 MEDLINE
DN 21283002 PubMed ID: 11279240
TI **TatB** and TatC form a functional and structural unit of the twin-arginine translocase from Escherichia coli.
AU Bolhuis A; Mathers J E; Thomas J D; Barrett C M; Robinson C
CS Department of Biological Sciences, University of Warwick, Coventry CV4 7AL, United Kingdom.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Jun 8) 276 (23) 20213-9.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200107
ED Entered STN: 20010716
Last Updated on STN: 20030105

Entered Medline: 20010712

L11 ANSWER 17 OF 18 MEDLINE
AB The Escherichia coli Tat system mediates Sec-independent export of protein precursors bearing twin arginine signal peptides. Genes known to be involved in this process include tatA, **tatB**, and tatC that form an **operon** with a fourth gene, tatD. The tatD gene product has two homologues in E. coli coded by the unlinked ycfH and yjjV genes. An E. coli strain with in-frame chromosomal deletions in all three of tatD, ycfH, and yjjV exhibits no significant defect in the cellular location of five cofactor-containing enzymes that are synthesized with twin arginine signal peptides. Neither these mutations nor overproduction of the TatD protein cause any discernible effect on the export kinetics of an additional E. coli Tat pathway substrate. It is concluded that proteins of the TatD family have no obligate involvement in protein export by the Tat system. TatD is shown to be a cytoplasmic protein. TatD binds to immobilized Ni(2+) or Zn(2+) affinity columns and exhibits magnesium-dependent DNase activity. Features of the tatA **operon** that may control TatD expression are discussed.
AN 2000287539 MEDLINE
DN 20287539 PubMed ID: 10747959
TI TatD is a cytoplasmic protein with DNase activity. No requirement for TatD family proteins in sec-independent protein export.
AU Wexler M; Sargent F; Jack R L; Stanley N R; Bogsch E G; Robinson C; Berks B C; Palmer T
CS Centre for Metalloprotein Spectroscopy and Biology, School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, United Kingdom.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Jun 2) 275 (22) 16717-22.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
ED Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000711

L11 ANSWER 18 OF 18 MEDLINE
AB We describe the identification of two Escherichia coli genes required for the export of cofactor-containing periplasmic proteins, synthesized with signal peptides containing a twin arginine motif. Both gene products are homologous to the maize HCF106 protein required for the translocation of a subset of lumenal proteins across the thylakoid membrane. Disruption of either gene affects the export of a range of such proteins, and a complete block is observed when both genes are inactivated. The Sec protein export pathway was unaffected, indicating the involvement of the gene products in a novel export system. The accumulation of active cofactor-containing proteins in the cytoplasm of the mutant strains suggests a role for the gene products in the translocation of folded proteins. One of the two HCF106 homologues is encoded by the first gene of a four cistron **operon**, tatABCD, and the second by an unlinked gene, tatE. A mutation previously assigned to the hcf106 homologue encoded at the tatABCD locus, mttA, lies instead in the **tatB** gene.
AN 1998315056 MEDLINE
DN 98315056 PubMed ID: 9649434
TI Overlapping functions of components of a bacterial Sec-independent protein export pathway.
AU Sargent F; Bogsch E G; Stanley N R; Wexler M; Robinson C; Berks B C; Palmer T
CS Nitrogen Fixation Laboratory, John Innes Centre, Colney, Norwich NR4 7UH.
SO EMBO JOURNAL, (1998 Jul 1) 17 (13) 3640-50.
Journal code: 8208664. ISSN: 0261-4189.
CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AJ005830
EM 199808
ED Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980821

=> s l5 and operon
L12 1 L5 AND OPERON

=> d kwic, bib, abs

L12 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI **Detection** of **virulence** genes in uropathogenic Escherichia coli by polymerase chain reaction (PCR): Comparison with results obtained using phenotypic methods.
AB . . . and phenotypically characterized. The strains were examined genotypically by using the polymerase chain reaction (PCR) for presence of five urovirulence **operons**: alpha-haemolysin (hly), cytotoxic necrotizing factor type 1 (cnf1), pyelonephritisassociated pili (pap), S. fimbriae (sfa) and afimbrial adhesin (afa). The phenotypic. . .
IT . . .
Molecular Biophysics)
IT Diseases
urinary tract infection: bacterial disease, community-acquired, urologic disease
IT Chemicals & Biochemicals
afimbrial adhesin [afa]: urovirulence **operon**; alpha-hemolysin [hly]: urovirulence **operon**; cytotoxic necrotizing factor type 1 [cnf 1]: urovirulence **operon**; pyelonephritis-associated pili [pap]: urovirulence **operon**; virulence genes; S. fimbriae [sfa]: urovirulence **operon**
AN 1998:122706 BIOSIS
DN PREV199800122706
TI **Detection** of **virulence** genes in uropathogenic Escherichia coli by polymerase chain reaction (PCR): Comparison with results obtained using phenotypic methods.
AU Blanco, M.; Blanco, J. E.; Rodriguez, E.; Abalia, I.; Alonso, M. P.; Blanco, J. (1)
CS (1) Reference Lab. E. Coli, Dep. Microbiol. Parasitol., Fac. Veterinary, Univ. Santiago de Compostela, 27002 Lugo Spain
SO Journal of Microbiological Methods, (Dec., 1997) Vol. 31, No. 1-2, pp. 37-43.
ISSN: 0167-7012.
DT Article
LA English
AB 102 Escherichia coli strains from patients with community-acquired urinary tract infections (UTIs) were genotypically and phenotypically characterized. The strains were examined genotypically by using the polymerase chain reaction (PCR) for presence of five urovirulence **operons**: alpha-haemolysin (hly), cytotoxic necrotizing factor type 1 (cnf1), pyelonephritisassociated pili (pap), S. fimbriae (sfa) and afimbrial adhesin (afa). The phenotypic methods used were: Vero and HeLa cells for detection of CNF1, blood agar for Hly and mannose-resistant haemagglutination typing for expression of adhesins. There was a very good correlation between the results obtained by PCR and those obtained by phenotypic methods. Thus, the PCR assays can by recommended for clinical use to detect uropathogenic E. coli strains, as well as for epidemiological studies.